

1 GTGTGCCGGA TTTGGTTAGC TGAGCCCACC GAGAGGCGCC TGCAGGATGA AAGCTCTCTG 60
1 M K A L C 5

61 TCTCCTCCTC CTCCTGTCC TGGGGCTGTT GGTGTCTAGC AAGACCCTGT GCTCCATGGA 120
6 L L L L P V L G L L V S S K T L C S M E 25

121 AGAAGCCATC AATGAGAGGA TCCAGGAGGT CGCCGGCTCC CTAATATTTA GGGCAATAAG 180
26 E A I N E R I Q E V A G S L I F R A I S 45

181 CAGCATTGGC CTGGAGTGCC AGAGCGTCAC CTCCAGGGGG GACCTGGCTA CTTGCCCCCG 240
46 S I G L E C Q S V T S R G D L A T C P R 65

241 AGGCTTCGCC GTCACCGGCT GCACTTGTGG CTCCGCCTGT GGCTCGTGGG ATGTGCGCGC 300
66 G F A V T G C T C G S A C G S W D V R A 85

301 CGAGACCACA TGTCAGTGCC AGTGCGCGGG CATGGACTGG ACCGGAGCGC GCTGCTGTCTG 360
86 E T T C H C Q C A G M D W T G A R C C R 105

361 TGTGCAGCCC TGAGGTCGCG CGCAGTGGCA ACAGCGCGGG CGGAGGCGGC TCCAGGTCCG 420
106 V Q P * 108

421 GAGGGTTGCG GGGGAGCTGG AAATAAACCT GGAGATGATG ATGATGATGA TGATGGAAAA 480

481 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 540

541 AAAAAAAAAA AAA 553

Figure 1

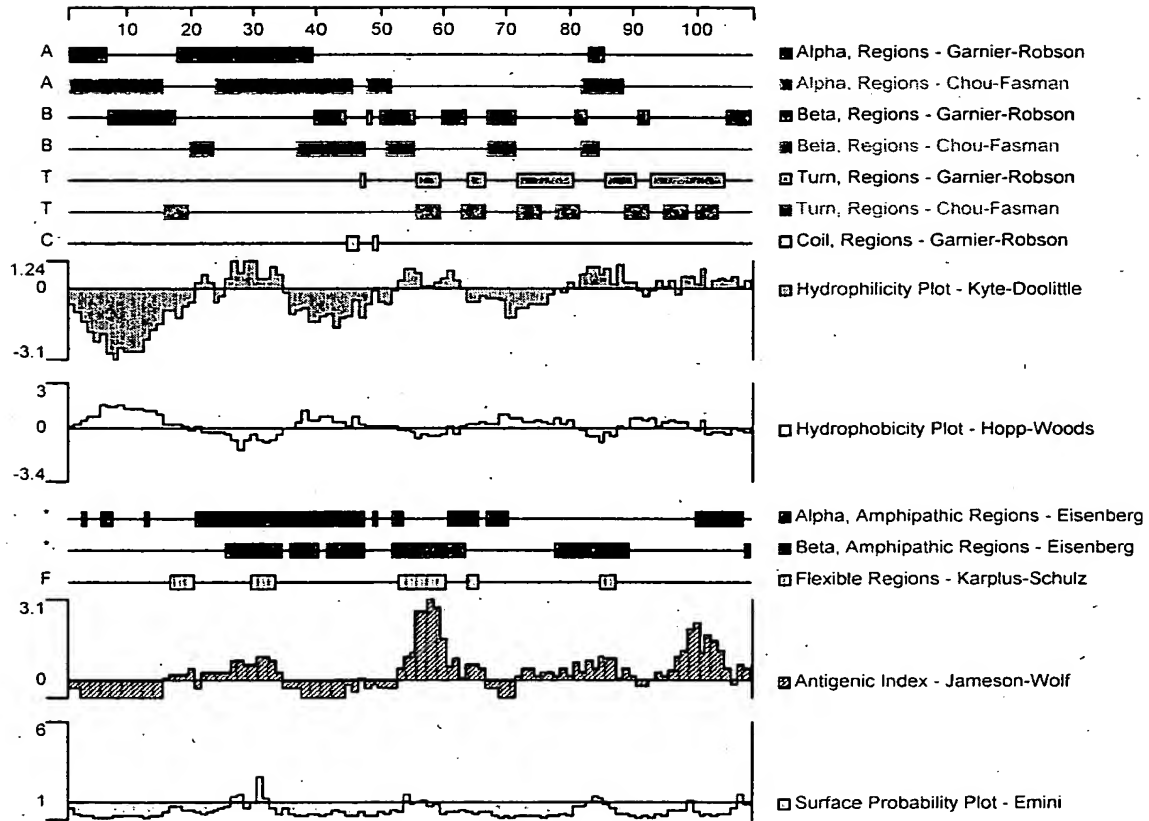


Figure 2